

**Table S1.**

ID	Group name	Targ	TP	FP	TN	FN	prec	Acc	MCC	Ranks		
										prec	Acc	MCC
170	DISOPRED3	53	359	130	13094	431	0.734	0.722	<b>0.559</b>	1	14	1
478	biomine_dr_mixed	53	347	196	13028	443	0.639	0.712	<b>0.507</b>	4	18	2
369	Prdos-CNF	53	313	163	13061	477	0.658	0.692	<b>0.489</b>	2	22	3
168	DisMeta	53	356	278	12946	434	0.562	0.715	<b>0.477</b>	5	16	4
216	POODLE	53	528	994	12230	262	0.347	0.797	<b>0.44</b>	9	1	5
288	biomine_dr_pdb_c	53	259	142	13082	531	0.646	0.659	<b>0.439</b>	3	28	6
222	MULTICOM-construct	53	489	1128	12096	301	0.302	0.767	<b>0.385</b>	13	4	7
129	CASPITAv2	52	405	833	12079	385	0.327	0.724	<b>0.364</b>	12	12	8
424	MULTICOM-novel	53	493	1299	11925	297	0.275	0.763	<b>0.363</b>	17	6	9
180	Yang-test	53	442	1055	12169	348	0.295	0.74	<b>0.358</b>	15	7	10
340	metaprdos2	48	448	1287	10578	246	0.258	0.769	<b>0.356</b>	19	3	11
115	Slbio	50	314	544	12062	426	0.366	0.691	<b>0.356</b>	8	23	12
214	OWL2	50	256	393	12027	438	0.394	0.669	<b>0.348</b>	6	27	13
003	GSmetsadisorderMD	50	389	932	11497	362	0.294	0.722	<b>0.342</b>	16	15	14
327	Espritzv2	53	332	626	12598	458	0.347	0.686	<b>0.341</b>	10	24	15
125	MULTICOM-refine	53	536	1821	11403	254	0.227	0.77	<b>0.333</b>	24	2	16
-	D2P2_Espritz-X	53	265	412	12812	525	0.391	0.652	<b>0.327</b>	7	29	17
413	ZHOU-SPARKS-X	53	528	1838	11386	262	0.223	0.765	<b>0.326</b>	25	5	18
193	Aldisorder	48	359	854	11043	392	0.296	0.703	<b>0.326</b>	14	21	19
-	D2P2_PrDOS	53	463	1528	11696	327	0.233	0.735	<b>0.311</b>	22	9	20
140	OnD-CRF2	53	432	1325	11899	358	0.246	0.723	<b>0.311</b>	21	13	21
380	Espritz	53	463	1682	11542	327	0.216	0.729	<b>0.294</b>	27	11	22
484	CSpritz	53	485	1881	11343	305	0.205	0.736	<b>0.29</b>	30	8	23
084	biomine_dr_pdb	53	403	1354	11870	387	0.229	0.704	<b>0.284</b>	23	20	24
496	GSmetsadisorder	53	420	1570	11654	370	0.211	0.706	<b>0.273</b>	28	19	25
273	IntFOLD2	53	562	3295	9929	228	0.146	0.731	<b>0.239</b>	34	10	26
-	D2P2_PV2	53	497	2668	10556	293	0.157	0.714	<b>0.236</b>	32	17	27
-	D2P2_IUPred-S	53	215	580	12644	575	0.27	0.614	<b>0.228</b>	18	32	28
***	Naïve	53	161	330	12894	629	0.328	0.589	<b>0.224</b>	11	33	29
-	D2P2_Espritz-N	53	289	1111	12113	501	0.206	0.641	<b>0.217</b>	29	31	30
183	sDisPred	53	474	3108	10116	316	0.132	0.682	<b>0.193</b>	36	25	31
384	GSmetsadisorder3d	51	167	486	12125	601	0.256	0.589	<b>0.193</b>	20	34	32
-	D2P2_VSL2b	53	355	2055	11169	435	0.147	0.647	<b>0.18</b>	33	30	33
494	GSmetsaserver	53	519	4005	9219	271	0.115	0.677	<b>0.175</b>	37	26	34
-	D2P2_IUPred-L	53	148	524	12700	642	0.22	0.574	<b>0.159</b>	26	36	35
-	D2P2_IUPred-A	53	112	492	12732	678	0.185	0.552	<b>0.119</b>	31	38	36
167	Algorithmic_code	53	265	2223	11001	525	0.107	0.584	<b>0.101</b>	38	35	37
-	D2P2_VLXT	53	236	2247	10977	554	0.095	0.564	<b>0.078</b>	39	37	38
-	D2P2_Espritz-D	53	78	496	12728	712	0.136	0.531	<b>0.071</b>	35	39	39

Comparison of CASP10 disorder predictors with the methods contributing to the D2P2 database on the common set of 53 CASP10 targets. The names of the database methods are precluded with the “D2P2” prefix. The groups are ranked according to the MCC score. The database methods are marked with the grey background.

**Table S2.**

ID	Group name	Targ	TP	FP	TN	FN	prec	Acc	MCC	AUC	Rank			
											prec	Acc	MCC	AUC
170	DISOPRED3	83	562	181	20636	817	0.756	0.699	<b>0.535</b>	<b>0.901</b>	1	20	<b>1</b>	<b>2</b>
369	Prdos-CNF	83	588	267	20550	791	0.688	0.707	<b>0.519</b>	<b>0.909</b>	2	18	<b>2</b>	<b>1</b>
478	biomine_dr_mixed	83	559	341	20476	820	0.621	0.694	<b>0.476</b>	<b>0.89</b>	4	22	<b>3</b>	<b>3</b>
288	biomine_dr_pdb_c	83	507	253	20564	872	0.667	0.678	<b>0.472</b>	<b>0.884</b>	3	25	<b>4</b>	<b>4</b>
168	DisMeta	83	551	361	20456	828	0.604	0.691	<b>0.465</b>	<b>0.691</b>	5	24	<b>5</b>	<b>32</b>
216	POODLE	83	901	1903	18914	478	0.321	0.781	<b>0.408</b>	<b>0.874</b>	12	1	<b>6</b>	<b>6</b>
222	MULTICOM-construct	83	857	1752	19065	522	0.328	0.769	<b>0.403</b>	<b>0.872</b>	11	4	<b>7</b>	<b>8</b>
129	CASPITAv2	82	778	1413	19092	601	0.355	0.748	<b>0.401</b>	<b>0.858</b>	9	8	<b>8</b>	<b>10</b>
340	metaprdos2	78	830	2004	17209	432	0.293	0.777	<b>0.385</b>	<b>0.879</b>	16	2	<b>9</b>	<b>5</b>
214	OWL2	79	496	623	19054	781	0.443	0.678	<b>0.38</b>	<b>0.819</b>	6	26	<b>10</b>	<b>19</b>
180	Yang-test	83	748	1519	19298	631	0.33	0.735	<b>0.374</b>	<b>0.873</b>	10	10	<b>11</b>	<b>7</b>
115	Sibio	76	553	868	18214	704	0.389	0.697	<b>0.373</b>	<b>0.71</b>	8	21	<b>12</b>	<b>31</b>
125	MULTICOM-refine	83	943	2753	18064	436	0.255	0.776	<b>0.357</b>	<b>0.844</b>	22	3	<b>13</b>	<b>15</b>
327	Espritzv2	83	695	1533	19284	684	0.312	0.715	<b>0.346</b>	<b>0.847</b>	13	16	<b>14</b>	<b>13</b>
424	MULTICOM-novel	83	856	2405	18412	523	0.263	0.753	<b>0.344</b>	<b>0.853</b>	20	7	<b>15</b>	<b>11</b>
193	Aldisorder	73	650	1464	16729	632	0.307	0.713	<b>0.34</b>	<b>0.819</b>	15	17	<b>16</b>	<b>20</b>
413	ZHOU-SPARKS-X	83	903	2752	18065	476	0.247	0.761	<b>0.34</b>	<b>0.87</b>	24	5	<b>17</b>	<b>9</b>
084	biomine_dr_pdb	83	742	1888	18929	637	0.282	0.724	<b>0.334</b>	<b>0.84</b>	19	12	<b>18</b>	<b>16</b>
003	GSmetsadisorderMD	76	693	1740	17207	605	0.285	0.721	<b>0.333</b>	<b>0.844</b>	18	14	<b>19</b>	<b>14</b>
380	Espritz	83	833	2518	18299	546	0.249	0.742	<b>0.326</b>	<b>0.852</b>	23	9	<b>20</b>	<b>12</b>
484	CSpritz	83	918	3197	17620	461	0.223	0.756	<b>0.318</b>	<b>0.827</b>	30	6	<b>21</b>	<b>17</b>
140	OnD-CRF2	82	725	2280	18500	613	0.241	0.716	<b>0.301</b>	<b>0.807</b>	25	15	<b>22</b>	<b>21</b>
496	GSmetsadisorder	83	801	2772	18045	578	0.224	0.724	<b>0.294</b>	<b>0.803</b>	29	13	<b>23</b>	<b>22</b>
***	Naïve	83	305	473	20344	1074	0.392	0.599	<b>0.26</b>	<b>0.798</b>	7	32	<b>24</b>	<b>23</b>
-	MobiDB_Dise-465	83	400	882	19935	979	0.312	0.624	<b>0.256</b>	<b>0.715</b>	14	29	<b>25</b>	<b>29</b>
273	IntFOLD2	83	1013	5599	15218	366	0.153	0.733	<b>0.246</b>	<b>0.822</b>	32	11	<b>26</b>	<b>18</b>
-	MobiDB_Espritz-X	83	515	1619	19198	864	0.241	0.648	<b>0.242</b>	<b>0.767</b>	26	27	<b>27</b>	<b>26</b>
-	MobiDB_IUPred-S	83	348	844	19973	1031	0.292	0.606	<b>0.227</b>	<b>0.64</b>	17	31	<b>28</b>	<b>34</b>
183	sDisPred	83	892	4966	15851	487	0.152	0.704	<b>0.224</b>	<b>0.769</b>	33	19	<b>29</b>	<b>24</b>
-	MobiDB_Espritz-N	83	448	1461	19356	931	0.235	0.627	<b>0.219</b>	<b>0.715</b>	27	28	<b>30</b>	<b>30</b>
494	GSmetsaserver	83	963	6466	14351	416	0.13	0.694	<b>0.198</b>	<b>0.768</b>	34	23	<b>31</b>	<b>25</b>
384	GSmetsadisorder3d	79	240	679	18899	1082	0.261	0.573	<b>0.174</b>	<b>0.758</b>	21	34	<b>32</b>	<b>27</b>
-	MobiDB_IUPred-L	83	255	828	19989	1124	0.235	0.573	<b>0.163</b>	<b>0.601</b>	28	35	<b>33</b>	<b>35</b>
-	MobiDB_Dise-HL	83	694	5623	15194	685	0.11	0.617	<b>0.125</b>	<b>0.652</b>	36	30	<b>34</b>	<b>33</b>
167	Algorithmic_code	83	511	3727	17090	868	0.121	0.596	<b>0.118</b>	<b>0.596</b>	35	33	<b>35</b>	<b>36</b>
-	MobiDB_Espritz-D	83	87	474	20343	1292	0.155	0.52	<b>0.062</b>	<b>0.753</b>	31	36	<b>36</b>	<b>28</b>

Comparison of CASP10 disorder predictors with the methods contributing to the MobiDB database on the common set of 83 CASP10 targets. The names of the database methods are precluded with the “MobiDB” prefix. The groups are ranked according to the MCC score. The database methods are marked with the grey background.